

GenCore version 5.1.5  
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 15:19:59 ; Search time 4955.25 Seconds  
(without alignments)  
11622.905 Million cell updates/sec

Title: US-09-625-573-3

Perfect score: 1979

Sequence: 1 CAGGACTGCGCTGAGACAAGC.....ATATGCAATATAAAATTTAG 1979

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

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15: em.ba.\*

16: em.fun.\*

17: em.hum.\*

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33: em.htg.mus.\*

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35: em.htg.rod.\*

36: em.htg.mam.\*

37: em.htg.vrt.\*

38: em.sy.\*

39: em.htgo.hum.\*

40: em.htgo.mus.\*

41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1979	100.0	1979	6	AR116075	AR116075 Sequence
2	1979	100.0	1979	6	I79543	I79543 Sequence 3
3	1979	100.0	1979	9	HSU03905	U03905 Human monoc
4	1943.8	98.2	5471	9	HS MCPA02	U0924 Human monoc
5	1943.8	98.2	143068	9	HSU35952	AX335952 Sequence
6	1943.8	98.2	143068	9	HSU95626	U95626 Homo sapien
7	1942.2	98.1	185437	9	AC098613	AC098613 Homo sapi
8	1702	86.0	2900	2	AC087602	AC087602 Pan trogl
9	1313	66.3	10528	6	AX345236	AX345236 Sequence
10	1286.4	65.0	10528	6	AX345237	AX345237 Sequence
11	1231.4	62.2	1651	9	HS MCP1REC	X93583 H.sapiens m
12	1083	54.7	1083	6	AX232508	AX232508 Sequence
13	1081.4	54.6	1083	6	AX232506	AX232506 Sequence
14	1081.4	54.6	1083	9	HUM MCP1R	D29884 Human mRNA
15	1079.8	54.6	1083	6	AX280849	AX280849 Sequence
16	1078.2	54.5	1083	6	E13909	E13909 cDNA encodi
17	1023.8	51.7	1083	9	AF013958	AF013958 Macaca mu
18	980	49.5	2232	6	AR116074	AR116074 Sequence
19	980	49.5	2232	6	I79542	I79542 Sequence 1
20	980	49.5	2232	9	HSU03882	U03882 Human monoc
21	780.6	39.4	1364	10	MMU51717	U51717 Mus musculu
22	777.4	39.3	2992	10	MMU56819	U56819 Mus musculu
23	775.8	39.2	1245	10	MMU47035	U47035 Mus musculu
24	769.8	38.9	1365	10	RNU77349	U77349 Rattus norv
25	712.6	36.0	1075	9	AF019379	AF019379 Cercopithec
26	711.8	36.0	1086	9	CAU83324	U83324 Cercopithec
27	711.8	36.0	1086	9	CAU83325	U83325 Cercopithec
28	711	35.9	1059	9	AF035222	AF035222 Cercopithec
29	711	35.9	1059	9	AF081577	AF081577 Cercopithec
30	710.2	35.9	1130	9	AF291669	AF291669 Macaca fa
31	709.4	35.8	1059	9	AF075448	U77672 Macaca mulla
32	708	35.8	1966	9	MMU77672	AF075448 Pygathrix
33	707.8	35.8	1059	9	AF005660	AF005660 Macaca fa
34	707.8	35.8	1059	9	AF035217	AF035217 Cercopithec
35	707.8	35.8	1059	9	AF075444	AF075444 Pygathrix
36	707.8	35.8	1059	9	AF141641	AF141641 Cercopithec
37	707.8	35.8	1059	9	AF212101	AF212101 Cercopithec
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## ALIGNMENTS

RESULT 1	1979 bp	DNA	Linear	PAT 16-MAY-2001
AR116075	AR116075	Sequence 3 from patent US 6132987.		
LOCUS	AR116075	GI:14096397		
DEFINITION	Sequence 3 from patent US 6132987.			
ACCESSION	AR116075			
VERSION	AR116075.1			
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 1979)			
AUTHORS	Charo, I.F. and Coughlin, S.R.			
TITLE	Recombinant mammalian monocytic chemotactic protein-1 (MCP-1) receptors (MCP-1R, CCR-2)			
JOURNAL	Patent: US 6132987-A 3 17-OCT-2000;			

FEATURES		Location/Qualifiers	
source	1..1979		
BASE COUNT	530 a 435 c 451 g 563 t		
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Best Local Similarity	100.0%; Pred. No. 0;		
Matches 1979; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 CAGGACTGCTGAGACAAGCCACAGCTGAACAGAGAAAGTGGAATGAACAGGACGGAT 60		
DB	1 CAGGACTGCTGAGACAAGCCACAGCTGAACAGAGAAAGTGGAATGAACAGGACGGAT 60		
QY	61 TTCGCCAGTACATCCACAAATGCTGCTCCATCTCGTTCTCGGTTTATCAGAAATACCA 120		
DB	61 TTCGCCAGTACATCCACAAATGCTGCTCCATCTCGTTCTCGGTTTATCAGAAATACCA 120		
QY	121 ACAGAGCGGTGAAGAGTACCACCTTTTGTGATATGATATAGGTACGGTGCTCCCTGTCTATA 180		
DB	121 ACAGAGCGGTGAAGAGTACCACCTTTTGTGATATGATATAGGTACGGTGCTCCCTGTCTATA 180		
QY	181 AATTGACGTGAAGCAATTTGGGCCCAACTCCCTGCCCTCTACTCGCTGGTGTTCA 240		
DB	181 AATTGACGTGAAGCAATTTGGGCCCAACTCCCTGCCCTCTACTCGCTGGTGTTCA 240		
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DB	241 TCTTTGGTTTGTGGCAACATGCTGCTGCTGCTCACTTAATAAATGCAAAAAGCTGA 300		
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DB	301 AGTGCTTGACTGACATTTACCTGCTCAACCTGGCCATCTCTGATCTGCTTTTCTTTATTA 360		
QY	361 CTCTCCCATTTGGGCTCACTCTGCTGCAAAATGAGTGGGCTTTTGGGAATGCAATGTCGA 420		
DB	361 CTCTCCCATTTGGGCTCACTCTGCTGCAAAATGAGTGGGCTTTTGGGAATGCAATGTCGA 420		
QY	421 AATTATTCAGGGCTGTATACATCGGTTATTTTGGCGGAATCTCTTCATCATCTCTCC 480		
DB	421 AATTATTCAGGGCTGTATACATCGGTTATTTTGGCGGAATCTCTTCATCATCTCTCC 480		
QY	481 TGACAATCGATAGTACCTGGCTATTTGCTCAATGAGTGGGCTTTTGGGAATGCAATGTCGA 540		
DB	481 TGACAATCGATAGTACCTGGCTATTTGCTCAATGAGTGGGCTTTTGGGAATGCAATGTCGA 540		
QY	541 TCACCTTTGGGPGGTGACAAGTGTATCACCTGGTGTGGTGTGCTGTGTTTGTCTGTCCTC 600		
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QY	601 CAGGAATCATCTTTACTAATGCCAGAAAGAGATCTGTTTATGTCGTGGGCCCTTTAT 660		
DB	601 CAGGAATCATCTTTACTAATGCCAGAAAGAGATCTGTTTATGTCGTGGGCCCTTTAT 660		
QY	661 TTCACAGGAGATGGAATAATTTCCACACAATATGAGGAACATTTTGGGCGTGGCTCCG 720		
DB	661 TTCACAGGAGATGGAATAATTTCCACACAATATGAGGAACATTTTGGGCGTGGCTCCG 720		
QY	721 CGCTGCTCATATGCTACTCTGCTACTCGGGAATCCTGAAAACCCCTGCTCGGTGTCGAA 780		
DB	721 CGCTGCTCATATGCTACTCTGCTACTCGGGAATCCTGAAAACCCCTGCTCGGTGTCGAA 780		
QY	781 ACGAGAAGAAGGATAGGGCAGTGAGATCATCTTCACCATCATGATGTTTACTTTC 840		
DB	781 ACGAGAAGAAGGATAGGGCAGTGAGATCATCTTCACCATCATGATGTTTACTTTC 840		
QY	841 TCTTCTGACTCCCTTATACATTTGTCATTCCTGGAACACCTTCAGGAATTTCTCGGCC 900		
DB	841 TCTTCTGACTCCCTTATACATTTGTCATTCCTGGAACACCTTCAGGAATTTCTCGGCC 900		
QY	901 TGAGTAACTGTGAAGACACCACTCAACTGGACCAAGCCACGCGACGAGACTCTTG 960		
DB	901 TGAGTAACTGTGAAGACACCACTCAACTGGACCAAGCCACGCGACGAGACTCTTG 960		

us-09-625-573-3.rge

Mon Jun 2'09:42:08 2003

DEFINITION	Sequence 3 from patent US 5707815.									
ACCESSION	I79543									
VERSION	I79543.1									
KEYWORDS	GI:3207833									
SOURCE	Unknown.									
ORGANISM	Unknown.									
REFERENCE	Unclassified.									
AUTHORS	1 (bases 1 to 1979)									
TITLE	Charo,I.F. and Coughlin,S.R.									
JOURNAL	Mammalian monocytic chemoattractant protein receptors and assays using them									
FEATURES	Patent: US 5707815-A 3 13-JAN-1998;									
source	Location/Qualifiers									
	1..1979									
BASE COUNT	530 a 435 c 451 g 563 t									
ORIGIN	/organism="unknown"									
	Query Match 100.0%; Score 1979; DB 6; Length 1979;									
	Best Local Similarity 100.0%; Pred. No. 0;									
	Matches 1979; Conservative 0; Mismatches 0; Indels 0; Gaps									
Qy	1	CAGGACTGCGCTGAGACAGCCACAAGCTGAACAGAGAAAGTGGATTGAACAGGACGCAT	60							
Db	1	CAGGACTGCGCTGAGACAGCCACAAGCTGAACAGAGAAAGTGGATTGAACAGGACGCAT	60							
Qy	61	TTCCCCAGTAGTACATCCACAACATGCTGTCCACATCTCGTTCTCGGTTTATCATGAATAACCA	120							
Db	61	TTCCCCAGTAGTACATCCACAACATGCTGTCCACATCTCGTTCTCGGTTTATCATGAATAACCA	120							
Qy	121	ACGAGAGCGGTGAAGAAGTCACACCTTTTTTGGATTATGATTACGGTGCCTCCGTGCATA	180							
Db	121	ACGAGAGCGGTGAAGAAGTCACACCTTTTTTGGATTATGATTACGGTGCCTCCGTGCATA	180							
Qy	181	AATTGTGACGTGAAGCAAAATTTGGGGCCCAACTCCTCGCTCGCTACTCGCTGGTGTTC	240							
Db	181	AATTGTGACGTGAAGCAAAATTTGGGGCCCAACTCCTCGCTCGCTACTCGCTGGTGTTC	240							
Qy	241	TCCTTTGGTTTTGTGGGCAACATGCTGGTGCCTCCTCAATCTATAAAGTGC	300							
Db	241	TCCTTTGGTTTTGTGGGCAACATGCTGGTGCCTCCTCAATCTATAAAGTGC	300							
Qy	301	AGTGTGTGACATGACATTTACCTGCTCAACCTGGCCATCTCTGATCTGCTTTTCTTATTA	360							
Db	301	AGTGTGTGACATGACATTTACCTGCTCAACCTGGCCATCTCTGATCTGCTTTTCTTATTA	360							
Qy	361	CTCTCCCAATTTGGGGTCACCTCTGCTCAAAATGAGTGGGTCTTTGGGAATGCAATGTGCA	420							
Db	361	CTCTCCCAATTTGGGGTCACCTCTGCTCAAAATGAGTGGGTCTTTGGGAATGCAATGTGCA	420							
Qy	421	AATTATTCACAGGGGTGTATCACAATCGGTTATTTTGGCGGAATCTTCTTCATCATCTCC	480							
Db	421	AATTATTCACAGGGGTGTATCACAATCGGTTATTTTGGCGGAATCTTCTTCATCATCTCC	480							
Qy	481	TCACAATCGATAGATACCTTGCTATTTGCCATGCTGTGTTGCTTTAAAGCCAGGACGG	540							
Db	481	TCACAATCGATAGATACCTTGCTATTTGCCATGCTGTGTTGCTTTAAAGCCAGGACGG	540							
Qy	541	TCACCTTTGGGGTGTGACAAAGTGTGATACCTGGTTGGTGGCTGTGTTGCTCTGTGCC	600							
Db	541	TCACCTTTGGGGTGTGACAAAGTGTGATACCTGGTTGGTGGCTGTGTTGCTCTGTGCC	600							
Qy	601	CAGGAATCATCTTTACTAAATGCCAGAAGAGATCTGTTTATGCTGTGGGCCCTTATT	660							
Db	601	CAGGAATCATCTTTACTAAATGCCAGAAGAGATCTGTTTATGCTGTGGGCCCTTATT	660							
Qy	661	TTCCACAGGATGGAATAAATTTCCACAATAATATGAGSAACATTTTGGGGCTGGTCTGTC	720							
Db	661	TTCCACAGGATGGAATAAATTTCCACAATAATATGAGSAACATTTTGGGGCTGGTCTGTC	720							
Qy	721	CGCTGCTCATATGGTCACTCTGCTACTCGGGAATCCTGAAACCCCTGCTTCGTGTCGAA	780							
Db	721	CGCTGCTCATATGGTCACTCTGCTACTCGGGAATCCTGAAACCCCTGCTTCGTGTCGAA	780							



Db	1201	TAACAATCTGATATAACAAACAACTTCAAGGGTTTGTGAACAATAGAAACCTGTAAAG	1260
Qy	1261	CAGGTGCCAGGAACCTCAGGGCTGTGTACTAATACAGACTATGTCAACCAATGCATA	1320
Db	1261	CAGGTGCCAGGAACCTCAGGGCTGTGTACTAATACAGACTATGTCAACCAATGCATA	1320
Qy	1321	TCCAACTATGCTCAGGGAATAATCCAGAAACCTGTGGGTAGAGACTTTGACTCTCCAG	1380
Db	1321	TCCAACTATGCTCAGGGAATAATCCAGAAACCTGTGGGTAGAGACTTTGACTCTCCAG	1380
Qy	1381	AAAGCTCATCTCAGCTCTGAAAATGCTCATTAACCTGTGCTTAATCTCTTTTCTAG	1440
Db	1381	AAAGCTCATCTCAGCTCTGAAAATGCTCATTAACCTGTGCTTAATCTCTTTTCTAG	1440
Qy	1441	TCTTCATATTTCTCACTCAATCTCTGATTTCTGCAATGCTTGAATCAAGGCCAGC	1500
Db	1441	TCTTCATATTTCTCACTCAATCTCTGATTTCTGCAATGCTTGAATCAAGGCCAGC	1500
Qy	1501	TGGAGTGAAGAAGAAATGTGACAGGCACAGATGAATGGGAGTGAGGATAGTGGGTC	1560
Db	1501	TGGAGTGAAGAAGAAATGTGACAGGCACAGATGAATGGGAGTGAGGATAGTGGGTC	1560
Qy	1561	AGGGCTGAGAGAGAGAGGAGACATGAGCATGCTGAGCTGGACAAACAAAGGT	1620
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Qy	1621	GAGCAAGGGCTCAGGCATTCAGCCAGGAGATGATCTGCTTACGCCCTATCTGCCAC	1680
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Qy	1681	GTGATTTAACTTGAAGGGTTCACAGCTCAGGAGAGTTTGGGAACCTGCAATAACCTG	1740
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Qy	1801	ATTACAGTTATCTATGGCAACCATGACATTTGAAATCTATGAAATATCATGCT	1860
Db	1801	ATTACAGTTATCTATGGCAACCATGACATTTGAAATCTATGAAATATCATGCT	1860
Qy	1861	CAATTGTTAGATGCTTCTAGCCACATCCCTCTGTAATAATTCAGAAAAATTTTGT	1920
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Qy	1921	TTATAAAGATGCTATCTATGATATGCTTAATATATGATATGCAATATAAATTTAG	1979
Db	1921	TTATAAAGATGCTATCTATGATATGCTTAATATATGATATGCAATATAAATTTAG	1979
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HSMPA02			
LOCUS	5471 bp	DNA	linear
DEFINITION	Human monocyte chemoattractant protein 1 receptor gene, two alternatively spliced forms, complete cds.		
ACCESSION	U80924		
VERSION	U80924.1	GI:1773032	
KEYWORDS			
SEGMENT			
SOURCE	2 of 2		
ORGANISM	Homo sapiens.		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 5471)		
AUTHORS	Wong, L.M., Myers, S.J., Tsou, C.L., Gosling, J., Arai, H. and Charo, I.F.		
TITLE	Organization and differential expression of the human monocyte chemoattractant protein 1 receptor gene. Evidence for the role of the carboxyl-terminal tail in receptor trafficking		
JOURNAL	J. Biol. Chem. 272 (2), 1038-1045 (1997)		
MEDLINE	97150864		
PUBMED	8995400		
REFERENCE	2 (bases 1 to 5471)		
AUTHORS	Myers, S.J. and Charo, I.F.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-DEC-1996) Pharmacology, Emory University, 1510 Clifton Road, Atlanta 30322, USA		
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/protein_id="AAC51636.1"			
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Query Match	98.2%	Score 1943.8;	DB 9; Length 5471;
Best Local Similarity	99.9%	Pred. No. 0;	
Matches 1945;	Conservative	0; Mismatches	2; Indels 0; Gaps 0;
Qy	27	CTGAACAGAGAAAGTGGATTGAACAAAGGACGACATTTCCCGAGTACATCCACAACATGCTG	86
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Qy	87	TCCACATCTCGTCTCGGTTTATCAGAAATACCAACAGAGCGGTGAAGAAGTACCACC	146
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Qy	207	CAACTCCCTCGCTCCGCTCTACTCGTGTGTTTCATCTTTTGGTTTGTGGCAACATGCTG	266
Db	1732	CAACTCCCTCGCTCCGCTCTACTCGTGTGTTTCATCTTTTGGTTTGTGGCAACATGCTG	1791
Qy	267	GTCGTCCTCATCTTAATAAAGTGCAGAAAGCTGAAGTCTTGCACATTTACCTGCTC	326
Db	1792	GTCGTCCTCATCTTAATAAAGTGCAGAAAGCTGAAGTCTTGCACATTTACCTGCTC	1851







Muzny,D., Chen,C.-N., Evans,C., FitzGerald,M., See,L.H., Tang,M., Porcel,B.M., Dragan,Y., Giacalone,J., Pae,A., Powell,E., Solinsky,K.A., Desilva,U., Diaz-Perez,S., Zhou,X., Yu,Y., Watanabe,M., Doggett,N., Garcia,D. and Sagripanti,J.-L.  
Human BAC clone 110P12  
Unpublished (1997)

# TITLE JOURNAL REFERENCE AUTHORS

2 (bases 1 to 143068)

McCombie,R.W., Wilson,R., Chen,E., Gibbs,R., Zuo,L., Johnson,D., Nhan,M., Parnell,L., Dedhia,N., Ansari,A., Mardis,E., Schuttz,K., Ghoj,L., de la Bastide,M., Kaplan,N., Greco,T., Touchman,J., Muzny,D., Chen,C.-N., Evans,C., FitzGerald,M., See,L.H., Tang,M., Porcel,B.M., Dragan,Y., Giacalone,J., Pae,A., Powell,E., Solinsky,K.A., Desilva,U., Diaz-Perez,S., Zhou,X., Yu,Y., Watanabe,M., Doggett,N., Garcia,D. and Sagripanti,J.-L.  
Direct Submission

## TITLE JOURNAL

Submitted (27-MAR-1997) Advanced Genome Analysis Course, Cold Spring Harbor Laboratory, 1Bungtown Rd., Cold Spring Harbor, NY 11724, USA

## COMMENT

Regions with single-strand coverage are as follows:

31434 - 31443 37900 - 37968 53303 - 53357  
59166 - 59206 63708 - 63998 65200 - 65335  
78605 - 78713 92135 - 92137 112377 - 112551  
112643 - 112778 134284 - 134309 134914 - 135019  
143046 - 144068.

## FEATURES

source

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Number U80924), two alternatively spliced mRNAs."  
/gene="ccr2"  
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chemoattractant protein 1 receptor (ccr2) alternatively  
spliced mRNA encoding A-form carboxyl tail, Accession  
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gene

mRNA

mRNA

CDS

CDS



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BASE COUNT 41194 a 30122 c 32403 g 39349 t
ORIGIN
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Best Local Similarity				99.9%;	Pred. No. 0;		
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## RESULT 7

## AC098613

## LOCUS

## DEFINITION

## AC098613

## AC098613

## VERSION

## AC098613.2

## KEYWORDS

## HTG.

## SOURCE

## human.

## ORGANISM

## Homo sapiens

## Eukaryotes

## Metazoa

## Chordata

## Craniata

## Vertebrata

## Euteleostomi

## Mammalia

## Primates

## Catarrhini

## Hominoidea

## Homo

## 1 (bases 1 to 185437)

## Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D.

## Direct Submission

## Unpublished

## 2 (bases 1 to 185437)

## Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.

## Direct Submission

## Submitted (26-OCT-2001)

## Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA

## 3 (bases 1 to 185437)

## Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D.

## Direct Submission

## Submitted (01-AUG-2002)

## Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA

## On Aug 1, 2002 this sequence version replaced gi:16445164.

## -----

## Genome Center

## Center: University of Washington Genome Center

## Center Code: UWGC

## Web site: http://www.genome.washington.edu

## Contact: uwgctg@u.washington.edu

## -----

## Project Information

## Center project name: chr-3

## Center clone name: RP11-24F11 (bc0137)

## -----

## Summary Statistics

## Sequencing vector: plasmid; L08752; 100% of reads

## Chemistry: Dye-terminator ET; 93% of reads

## Chemistry: Dye-terminator Big Dye; 7% of reads

## Assembly program: Phrap; version 0.990319

## Consensus quality: 184860 bases at least Q40

## Consensus quality: 185398 bases at least Q30

## Consensus quality: 185435 bases at least Q20

## Insert size: 185437; sum-of-contigs

## Quality coverage: 7.6x in Q20 bases; sum-of-contigs

## -----

## Overlapping Sequences:

## 5': BAC-110P12 U95626, 111014-bp overlap

## 3': RP11-509121 (UWGC:bc0454) AC104304, 61294-bp overlap

## -----

## Sequence Quality Assessment:

## This entry has been annotated with sequence quality

## estimates computed by the Phrap assembly program.

## All manually edited bases have been reduced to quality zero.

## Quality levels above 40 are expected to have less than

## 1 error in 10,000 bp.

## Base-by-base quality values are not generally visible from the

## GenBank flat file format but are available as part

## of this entry's ASN.1 file.

## -----

## This sequence was finished as follows unless otherwise noted:

## all regions were either double-stranded or sequenced with an

## alternate chemistry or covered by high quality data (i.e., Phred

quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

## Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

BgIII				ECORI				HindIII			
SeqDerMap	EngPrnt	SeqDerMap	EngPrnt	SeqDerMap	EngPrnt	SeqDerMap	EngPrnt	SeqDerMap	EngPrnt	SeqDerMap	EngPrnt
11786	12040	8696	8837	9531	9423						
2067	2065	6	<800	6382	6501						
5681	5720	1846	1824	512	<800						
3716	3953	4052	3986	449	<800						
875	897	1159	1130	6692	6501						
910	897	54	<800	10449	10229						
2169	2215	560	<800	953	1025						
1705	1653	2287	2267	3124	3176						
5763	5720	4905	4891	1054	1025						
5844	5720	3049	3078	3985	3998						
5061	5001	1377	1394	1100	1025						
2625	2640	9903	9772	124	<800						
725	<800	1022	1021	2671	2693						
1173	1161	12606	12503	1948	1968						
5747	5720	866	868	83	<800						
9995	9684	9817	9772	7455	7474						
999	999	3598	3601	1305	1267						
4541	4503	452	<800	1047	1025						
2950	2981	7549	7635	3299	3301						
406	<800	2063	2075	5279	5237						
3375	3602	5837	5858	6815	6926						
13024	13045	13685	13328	435	<800						
416	<800	4104	3986	2509	2576						
10298	10140	1943	1928	2218	2172						
1478	1452	3964	3986	3797	3802						
287	<800	2758	2771	7758	7830						

[illegible]

TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	COMMENT
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COMMENT

Genome Center

Center project name: ZUAC

Center project name: ZUAC  
Center clone name: PP43-177M19

Center clone name: RP43-177M18

## Summary Statistics

Sequencing vector: M13; L08821

Chemistry: Dye-primer Bodipy:

**Chemistry:** Dye-terminator Big

Assembly program: Phrap: version

Assembly program: Phrap; version:  
Consensus quality: 15117 bases

Consensus quality:	15117 bases
Consensus quality:	28463 bases

Consensus quality: 28463 bases

Consensus quality: 43561 bases

Estimated insert size: 21502; ...

Quality coverage: 0x in Q20 band

Quality coverage: 0.1x in Q20

-----

TE: Estimated insert size may vary.

WE: Estimated insert size may  
(see <http://www.hasc> bcm tmc ec

(see <http://www.hgsc.bcm.tmc.edu>)

TE: This is a 'working draft' s

\_\_\_\_\_

\* consists of 1 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 2900: contig of 2900 bp in length.

FEATURES  
source

Location/Qualifiers  
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/db\_xref="taxon:9598"  
/clone="RP43-177M18"  
BASE COUNT 808 a 656 c 633 g 803 t

Query Match 86.0%; Score 1702; DB 2; Length 2900;

Best Local Similarity 96.8%; Pred. No. 0; Mismatches 55; Indels 3; Gaps 3;  
Matches 1768; Conservative 0

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QY	451	ATTTTGGCGGAATCTTCTTCATCATCTCTGACATCGATAGATACCTGGCTATTGTCC	510
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QY	571	CCTGGTGTGGCTGTGTTTGGCTTCTGTCGCCAGGAATCATCTTTACTAAATGCCAGAAAG	630
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QY	751	GAATCCTGAAACCCCTGCTCGGTGTGAAACAGAGAGAGAGATAGGCGAGTGAGAG	810
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QY	811	TCATCTTCAACATCATGATGTTTACTTCTTCTCTGCTGCTCATCATGTCATCTGCTACTCGG	870
Db	1949	TCATCTTCAACATCATGATGTTTACTTCTTCTCTGCTGCTCATCATGTCATCTGCTACTCGG	1890
QY	871	TCCTGAAACACCTTCCAGGAATCTTGGCCCTGAGTAACTGTGAAAGCAGCAGTCAACTGG	930
Db	1889	TCCTGAAACACCTTCCAGGAATCTTGGCCCTGAGTAACTGTGAAAGCAGCAGTCAACTGG	1830
QY	931	ACCAAGCCAGCGAGTGACAGAGACTCTTGGGATGACTCTGCTGCTCATCAATCCCATCA	990

Db	1829	ACCAAGCCAGCGAGTGACAGAGACTCTTGGGATGACTCTGCTCATCAATCCCATCA	1770
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Db	1289	TTCTGTCAATGTCTTTGAAATCAAGGGCCAGCTGGAGTGAAGAGAAATGTGACAGCA	1230
QY	1530	CAGATGAATGGAGTGGAGGATAGTGGGTCAAGGCTGAGAGGAGAGAGGAGACATG	1589
Db	1229	CAGATGAATGGAGTGGAGGATAGTGGGTCAAGGCTGAGAGGAGAGAGGAGACATG	1170
QY	1590	AGCATGCTGAGCCTGGACAAAGACAAGGTGAGCAAAAGGCTCAGCGATTCAGCCAGGA	1649
Db	1169	AGCATGCTGAGCCTGGACAAAGACAAGGTGAGCAAAAGGCTCAGCGATTCAGCCAGGA	1110
QY	1650	GATGATGCTGCTCTAGCCC-CATCTGCCACGTGTATTTAACTTTGAAGGTTTCAACAG	1708
Db	1109	GATAATGCTGCTTAGCCCGCATCTGCCACGTGTATTTAACTTTGAAGGTTTCAACAG	1050
QY	1709	GTCAGGAGAGCTTTGGGAACCTGCAATTAACCTGGAGTTTGTGGAGTCCG-ATGATTTCT	1767
Db	1049	GTCAGGAGAGCTTTGGGAACCTGCAATTAACCTGGAGTTTGTGGAGTCCGATGATCT	990
QY	1768	CTTTTGCATAAGTGCATACATATTTTGTCTTATACAGTTTATCTATGGCACCCTATGC	1827
Db	989	CTTTTGCATAAGTGCATACATATTTTGTCTTATACAGTTTATCTATGGCACCCTATGC	930
QY	1828	ACCTTACATTTGAATCTATGAATATCATGCTCCATGTTTTCAGATGCTTCTTAGGCCAC	1887
Db	929	ACCTTACATTTGAATCTATGAATATCATGCTCCATGTTTTCAGATGCTTCTTAGGCCAC	870
QY	1888	ATCCCCCTGTCTAAATAATTCAGAAATTTTGTCTTATAAAGATGCTATCTATGATAT	1947
Db	869	ATCCCCCTGTCTAAATAATTCAGAAATTTTGTCTTATAAAGATGCTATCTATGATAT	810
QY	1948	GCTAATATATGATATGCAATATAA 1973	
Db	809	GCTAATATATGATATGCAATATAA 784	

RESULT 9

AX345236	AX345236	10528 bp	DNA	linear	PAT 01-FEB-2002
LOCUS	Sequence 307 from Patent WO0200928.				
DEFINITION	Sequence 307 from Patent WO0200928.				
ACCESSION	AX345236				
VERSION	AX345236.1	GI:18493122			
KEYWORDS					
SOURCE	synthetic construct.				
ORGANISM	synthetic construct				
	artificial sequences.				
REFERENCE	1				
AUTHORS	Olek A., Piepenbrock C. and Berlin K.				
TITLE	Diagnosis of diseases associated with the immune system				
JOURNAL	Patent: WO 0200928-A 307 03-JAN-2002;				
	EpiGenomics AG (DE)				
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source	1..10528				
	/organism="synthetic construct"				
	/db_xref="taxon:32630"				
	/note="chemically treated genomic DNA (Homo sapiens)"				
BASE COUNT	3072 a 86 c 2419 g 4951 t				
ORIGIN					
Query Match	66.3%; Score 1313; DB 6; Length 10528;				
Best Local Similarity	79.7%; Pred. No. 0;				
Matches 1550; Conservative	0; Mismatches 395; Indels 0; Gaps 0;				
QY 29	GAACAGAGAAGTGGATTGAACAGGACGATATCCCGAGTACATCCACAAACATGCTGTC 88				
Db 8327	GAATAGAGAAGTGGATTGAATAGGACGATATTTTAGTATATTTAAATATGTTGT 8386				
QY 89	CACATCTCGTCTCGGTTATTCAGAAATACCAACGAGAGCGGTGAAGAAGTCACACCTT 148				
Db 8387	TATATTCGTTTCGGTTTATTAGAAATATTACGAGAGCGGTGAAGAAGTATTATT 8446				
QY 149	TTTTGATTATGATTACCGTGTCCCTGTCAATAAATTGACGTGAAGCAAAATGGGGCCCA 208				
Db 8447	TTTTGATTATGATTACCGGTGTTCCTGTATATAAATTCACGTGAAGTAAATTTGGGGTTA 8506				
QY 209	ACTCCTGCCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTTGGGCAACATCGTGT 268				
Db 8507	ATTTTGTGTTTCGTTTATTTCGTTGGTGTATTTTTGGTTTTGGGTAATATGTTGT 8566				
QY 269	CGPCCCTCACTTAATAAAGTCAAAAGCTGAAGTGTGACTGACATTTACCTGCTCAA 328				
Db 8567	CGTTTTTATTTAAATAATGTAAAGTTGAAGTGTGATTGATATTTATTTGTTTAA 8626				
QY 329	CCTGGCCATCTCTGATCTGCTTTTCTTATTAATCTCCATGTTGGCTCACTCTGCTGC 388				
Db 8627	TTTGGTTATTTTGAATGTTTTTTTATTATTTTTTATGTTGGGTTATTATTGTTGT 8686				
QY 389	AAATGAGTGGGCTTTGGGAATCAATGTGCAAAATATTACAGGGCTGTATCATCGG 448				
Db 8687	AAATGAGTGGGCTTTGGGAATCAATGTGCAAAATATTATAGGGTGTATTATATCGG 8746				
QY 449	TTATTTGGCGGAATCTTCTTCATCATCCCTCCGACATCGATAGATACCTGGCTATTGT 508				
Db 8747	TTATTTGGCGGAATTTTTTTTATTAATTTTTTGAATAATCGATAGATATTGGTTATTGT 8806				
QY 509	CCATCGTGTGTTGCTTTAAAGCCAGGACGGTCACTTTGGGGTGGTGACAAAGTGTGAT 568				
Db 8807	TTATCTGTGTTGTTGTTTTAAAGTTAGGACGGTTATTTTGGGGTGGTGATAGTGTAT 8866				
QY 569	CACCTGTTGGGCTGTGTTTTCCTCTGCTCCAGGAATCATCTTACTAAATGCCAGAA 628				
Db 8867	TATTTGGTGGGCTGTGTTTTCCTCTGCTCCAGGAATCATCTTACTAAATGCCAGAA 8926				
QY 629	AGAGATTCTGTTTATGCTGTGGGCCCTTATTTCCACGAGGATGGAATAATTTCCACAC 688				
Db 8927	AGAAGATTCTGTTTATGTTTGGTGTTTTATTTTACAGGATGGAATAATTTTATAT 8986				
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1641 CAGCAGGAGATGATCTGGTCTCTAGCCCATCTGCCACGCTGATTTAAACCTTGAAGGG 1700  
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 1021 TGATCTCTTTGCAATAGTGCATGACATATTTTGGCTTTATTAACAGTTTATCTATGGCA 1080  
 1821 CCATGACCTTACATTTGAAATCTATGAATATATCATGCTCCATGTTCCAGATGCTTCT 1880  
 1081 CCATGACCTTACATTTGAAATCTATGAATATATCATGCTCCATGTTCCAGATGCTTCT 1140  
 1881 AGGCCACATCCCTGCTCAAAAATTCAGAAAATTTTCTTTATTAAGATGCAATATCT 1940  
 1141 AGGCCACATCCCTGCTCAAAAATTCAGAAAATTTTCTTTATTAAGATGCAATATCT 1200  
 1941 ATGATATGCTAATATATGATATGCAATATATA 1973  
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RESULT 12  
 AX232508 1083 bp DNA linear PAT 11-SEP-2001  
 LOCUS Sequence 3 from Patent WO0162796.  
 DEFINITION AX232508  
 ACCESSION AX232508.1 GI:15592570  
 VERSION  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1083)  
 Valdes A.M., Groot P.H. and Spurr N.K.  
 Ccr2-641, polymorphic variant of the human ccr2 receptor and its  
 use in the diagnostic and treatment of atherosclerosis  
 Patent: WO 0162796-A 3 30-AUG-2001;  
 JOURNAL SMITHKLINE BEECHAM PLC (GB)  
 FEATURES Location/Qualifiers  
 source i.1083  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 255 a 260 c 247 g 321 t  
 ORIGIN

Query Match 54.78; Score 1083; DB 6; Length 1083;  
 Best Local Similarity 100.0%; Pred. NO. 6.2e-287; Indels 0; Gaps 0;  
 Matches 1083; Conservative 0; Mismatches 0

81 ATGCTGTCACATCTCGTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAGTC 140  
 1 ATGCTGCCACATCTCGTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAGTC 60  
 141 ACCACCTTTTGTATGATGATAGTACGGTCTCCCTGTCATAAATTTGACGTGAAGCAAT 200  
 61 ACCACCTTTTGTATGATGATGATAGTACGGTCTCCCTGTCATAAATTTGACGTGAAGCAAT 120  
 201 GGGGCCCAACTCCTCGCTCCGCTCTACCTCGCTGGGTGTTCACTTTTGGTGGGCAAC 260  
 121 GGGGCCCAACTCCTCGCTCCGCTCTACCTCGCTGGGTGTTCACTTTTGGTGGGCAAC 180  
 261 ATGCTGGTGGTCTCATCTTATAAATCACTGCAAAAAGCTGAAGTGTGCTGACATTTAC 320  
 181 ATGCTGGTGGTCTCATCTTATAAATCACTGCAAAAAGCTGAAGTGTGCTGACATTTAC 240  
 321 CTGCTCAACCTGGCCATCTCTGATCTGCTTTTCTTATTAACCTGCTGCTGCTGCTAC 380  
 241 CTGCTCAACCTGGCCATCTCTGATCTGCTTTTCTTATTAACCTGCTGCTGCTGCTAC 300

381 TCTGCTGCAATGAGTGGTCTTGGGAATGCAATGCAAAATTTATTCACAGGCTGTAT 440  
 301 TCTGCTGCAATGAGTGGTCTTGGGAATGCAATGCAAAATTTATTCACAGGCTGTAT 360  
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 361 CACATCGGTTATTTTGGCGGAATCTTCTTCATCATCTCTGACAAATCGATAGTACCTG 420  
 501 GCTATTGTCATGCTGCTGTTTGAAGCCAGACAGGCTCACCCTTGGGGTGGTGACA 560  
 421 GCTATTGTCATGCTGCTGTTTGAAGCCAGACAGGCTCACCCTTGGGGTGGTGACA 480  
 561 AGTGTGATCACCCTGTTGGTGGTCTTCTGTCCTCCAGGAATCATCTTTACTATAA 620  
 481 AGTGTGATCACCCTGTTGGTGGTCTTCTGTCCTCCAGGAATCATCTTTACTATAA 540  
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 601 TTCCACACAATATGAGGAACATTTGGGCTGTCCTCGCTGCTCATCATCTGTCATC 660  
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 1081 TAA 1083

RESULT 13  
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 LOCUS Sequence 1 from Patent WO0162796.  
 DEFINITION AX232506  
 ACCESSION AX232506  
 VERSION AX232506.1 GI:15592569  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1083)  
 Valdes A.M., Groot P.H. and Spurr N.K.  
 Ccr2-641, polymorphic variant of the human ccr2 receptor and its  
 use in the diagnostic and treatment of atherosclerosis  
 Patent: WO 0162796-A 3 30-AUG-2001;  
 JOURNAL SMITHKLINE BEECHAM PLC (GB)  
 FEATURES Location/Qualifiers  
 source i.1083  
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 /db\_xref="taxon:9606"  
 BASE COUNT 255 a 260 c 247 g 321 t  
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JOURNAL Patent: WO 0162796-A 1 30-AUG-2001;

SMITHKLINE BEECHAM PLC (GB)

Location/Qualifiers

source

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/organism="Homo sapiens"

/db\_xref="taxon:9606"

BASE COUNT 256 a 260 c 246 g 321 t

ORIGIN

Query Match 54.6%; Score 1081.4; DB 6; Length 1083;  
Best Local Similarity 99.9%; Pred. No. 1.7e-286;  
Matches 1082; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 81 ATGCTGTCCATCTCGTTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTC 140  
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QY 201 GGGGCCCAACTCTGCTCGCTCTACTCGCTGCTGTTTCATCTTTGTTTGTGGGCAAC 260  
Db 121 GGGGCCCAACTCTGCTCGCTCTACTCGCTGCTGTTTCATCTTTGTTTGTGGGCAAC 180

QY 261 ATGCTGTGCTCTCTCATCTTAATAACTGCAAAAGCTGAAGTCTTGACTGACATTTAC 320  
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QY 321 CTGCTCAACTGGCCATCTCTGATCTGCTTTTCTTATTACTCTCCATTTGGGCTCAC 380  
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QY 381 TCTGCTGCAATGAGTGGTCTTTGGGAATGCAATGTCAAAATTTACAGGCTGTAT 440  
Db 301 TCTGCTGCAATGAGTGGTCTTTGGGAATGCAATGTCAAAATTTACAGGCTGTAT 360

QY 441 CACATCGGTATTATTTGGCGGAATCTTCTCATCATCTCTCTGACATCTGATACCTG 500  
Db 361 CACATCGGTATTATTTGGCGGAATCTTCTCATCATCTCTCTGACATCTGATACCTG 420

QY 501 GCTATTGCCATGCTGTGTTCTTTAAAGCCAGGAGCTACCTTTGGGGTGGTGACA 560  
Db 421 GCTATTGCCATGCTGTGTTCTTTAAAGCCAGGAGCTACCTTTGGGGTGGTGACA 480

QY 561 AGTGTGATCAGCTGTTGGTGGCTGTTGCTTCTGCTCCAGGAATCATCTTTACTAA 620  
Db 481 AGTGTGATCAGCTGTTGGTGGCTGTTGCTTCTGCTCCAGGAATCATCTTTACTAA 540

QY 621 TGCCAGAAAGAAATCTGTTTATGCTGTGGCCCTTATTTCCAGGAGATGGATAAT 680  
Db 541 TGCCAGAAAGAAATCTGTTTATGCTGTGGCCCTTATTTCCAGGAGATGGATAAT 600

QY 681 TTCCACACAATTAAGAGAAACATTTTGGGGTGGTCTGCTGCTCATCATGTCATC 740  
Db 601 TTCCACACAATTAAGAGAAACATTTTGGGGTGGTCTGCTGCTCATCATGTCATC 660

QY 741 TGCTACTCGGGAATCCTGAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800  
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QY 921 AGTCAACTGGACCAAGCCAGGCTGACAGAGACTCTTGGGATGACTCACTGCTGCTGCT 980  
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QY 981 AATCCCATCATCTATGCTTCGTTGGGAGAAAGTTCAGAAAGTATCTCTCGTGTCTTC 1040  
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QY 1101 GATGGAGTCACTTCAACAACACGCTTCCACTGGGAGCAGGAGTCTCGGCTGGTTTA 1160  
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QY 1161 TAA 1163  
Db 1081 TAA 1083

RESULT 14  
HUMMCP1R  
LOCUS  
DEFINITION Human mRNA for monocyte chemoattractant protein 1 receptor (MCP-1 receptor), complete cds.  
ACCESSION D29984  
VERSION D29984  
KEYWORDS G-protein-coupled seven-transmembrane-type receptor; MCP-1 receptor; monocyte chemoattractant protein 1 receptor.  
SOURCE Homo sapiens monocyte cell-line THP-1 cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (sites)  
AUTHORS Yamagami,S., Tokuda,Y., Ishii,K., Tanaka,H. and Endo,N.  
TITLE cDNA cloning and functional expression of a human monocyte chemoattractant protein 1 receptor  
JOURNAL Biochem. Biophys. Res. Commun. 202 (2), 1156-1162 (1994)  
MEDLINE 94324942  
REFERENCE 2 (bases 1 to 1083)  
AUTHORS Yamagami,S.  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 1083)  
AUTHORS Yamagami,S.  
TITLE Direct Submission  
JOURNAL Submitted (22-APR-1994) Shinsuke Yamagami, TEIJIN LIMITED, Institute for Bio-Medical Research; 4-3-2 Asahigaoka, Hino, Tokyo 191, Japan (Tel:0425-86-8282)  
COMMENT Submitted (22-Apr-1994) to DDBJ by: Shinsuke Yamagami Teijin Limited Institute for Bio-Medical Research 4-3-2 Asahigaoka Hino, Tokyo 191 Japan  
Phone: 0425-86-8282  
Fax: 0425-87-5512.

## FEATURES

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## CDS

255 a 259 c 247 g 322 t  
BASE COUNT

Query Match	54.6%	Score 1081.4	DB 9	Length 1083
Best Local Similarity	99.9%	Pred. No. 1.7e-286		
Matches 1082	Conservative	0	Mismatches 1	Indels 0
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QY	261	ATGCTGTGTCGTCATCTTTAAATAAATGCAAAAGCTGAAGTGCTTGACTGACATTTAC	320	
DB	181	ATGCTGTGTCGTCATCTTTAAATAAATGCAAAAGCTGAAGTGCTTGACTGACATTTAC	240	
QY	321	CTGCTCAACCTGGCCATCTCTGATCTGCTTTTCTTATTAATCTCTCCATTTGGGGCTCAC	380	
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QY	381	TCTGCTCAAAATGAGTGGGTCTTTGGAAATGCAATGTGCAAAATTTACACAGGGCTGTAT	440	
DB	301	TCTGCTCAAAATGAGTGGGTCTTTGGAAATGCAATGTGCAAAATTTACACAGGGCTGTAT	360	
QY	441	CACATCGGTTATTTTGGGGAAATCTTCTCATCATCTCTGACAAATCGATACATACCTG	500	
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QY	501	GCTATGTCCATGCTGTGTTGTTTTAAAGCCAGGACGGTCACCTTTGGGGTGGTGACA	560	
DB	421	GCTATGTCCATGCTGTGTTGTTTTAAAGCCAGGACGGTCACCTTTGGGGTGGTGACA	480	
QY	561	AGTGTGATPACCTGGTTGGTGGCTGTGTTTGTTCTGTGCCAGGAATCATCTTTACTHAAA	620	
DB	481	AGTGTGATPACCTGGTTGGTGGCTGTGTTTGTTCTGTGCCAGGAATCATCTTTACTHAAA	540	
QY	621	TGCCAGAAGAAGATCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT	680	
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QY	681	TTCCACACAATAATGAGGAACATTTTGGGGCTGGTCTCGCGCTCATCATNGGTCATC	740	
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Db	1081	TAA	1083				
RESULT 15							
AX280849							
LOCUS	AX280849		1083 bp	DNA	linear	PAT 02-NOV-2001	
DEFINITION	Sequence	472 from Patent WO01/77172.					
ACCESSION	AX280849						
VERSION	AX280849.1	GI:16608180					
KEYWORDS							
SOURCE	human.						
ORGANISM	Homo sapiens						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
TITLE	1	Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.L.					
JOURNAL	Non-endogenous, constitutively activated known g protein-coupled						
FEATURES	receptors						
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	Arene Pharmaceuticals, Inc. (US)						
	Location/Qualifiers						
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ORIGIN							
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	Best Local Similarity	99.8%;	Pred. No. 4.7e-286;				
	Matches 1081;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;		
QY	81	ATGCTGTCACATC	TGCTCGGTTTATCAGAAATACCAACGAGAGCGGTG	NAGAAGTC	140		
Db	1	ATGCTGTCACATC	TGCTCGGTTTATCAGAAATACCAACGAGAGCGGTG	NAGAAGTC	60		
QY	141	ACCACCTTTT	TGATTATGATTACGCTGCTCCCTGTCATAAATTTGACGTTGAAGCAAAAT	200			
Db	61	ACCACCTTTT	TGATTATGATTACGCTGCTCCCTGTCATAAATTTGACGTTGAAGCAAAAT	120			
QY	201	GGGGCCCAACT	CTCGCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGGGGCAAC	260			
Db	121	GGGGCCCAACT	CTCGCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGGGGCAAC	180			
QY	261	ATGCTGGTCTGCT	CTCATTTAATAAACTGCAAAAAGCTGAAGTGCCTTGACTGCACATTTAC	320			
Db	181	ATGCTGGTCTGCT	CTCATTTAATAAACTGCAAAAAGCTGAAGTGCCTTGACTGCACATTTAC	240			
QY	321	CTGCTCAACT	CGCCATCTCTGATCTGCTTTTCTTTATTACTCTCCCAATTTGGGGCTCAC	380			
Db	241	CTGCTCAACT	CGCCATCTCTGATCTGCTTTTCTTTATTACTCTCCCAATTTGGGGCTCAC	300			
QY	381	TCCTGCTGCAAA	TGAGTGGGTCTTTGGGAATGCAATGTGCAAAATTTTCACAGGCGCTGAT	440			
Db	301	TCCTGCTGCAAA	TGAGTGGGTCTTTGGGAATGCAATGTGCAAAATTTTCACAGGCGCTGAT	360			
QY	441	CACATCGGTTAT	TTTGGCGGAATCTCTTCATCATCTCTCGCAATCGATAGATACCTG	500			
Db	361	CACATCGGTTAT	TTTGGCGGAATCTCTTCATCATCTCTCGCAATCGATAGATACCTG	420			
QY	501	GCTATTGTCCAT	CGCTGTGTTTGCTTTTAAAAAGCCAGGAGCGGTTCACCTTTGGGGTGGTGACA	560			
Db	421	GCTATTGTCCAT	CGCTGTGTTTGCTTTTAAAAAGCCAGGAGCGGTTCACCTTTGGGGTGGTGACA	480			
QY	561	AGTGTGATCATC	CGTGGTGGGTGTGTTTGTCTCTCCGAGGAATCATCTTTACTAAA	620			
Db	481	AGTGTGATCATC	CGTGGTGGGTGTGTTTGTCTCTCCGAGGAATCATCTTTACTAAA	540			

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Job time : 5316.25 secs